

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:43:19 ; Search time 2351.15 Seconds

(Without alignments)
168.399 Million cell updates/sec

Title: US-09-851-670-2

Sequence: 1 cgacaataatgaaaaaacagctgcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
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7: gb_ph: *
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13: gb_un: *
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27: em_sy: *
28: em_un: *
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30: em_htgo_hum: *
31: em_htgo_inv: *
32: em_htgo_rnd: *
33: em_htg_hum: *
34: em_htg_inv: *
35: em_htg_rnd: *
36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.6	60.8	42	6	121514	121514 Sequence 61
2	14.6	60.8	58	6	A42718	A42718 Sequence 50
3	14.6	60.8	58	6	187224	187224 Sequence 50
4	14.4	60.0	51	6	AX161485	AX161485 Sequence
5	14.2	59.2	42	6	E31994	E31994 Process for
6	14.2	59.2	57	9	HUMACTGAM	K00791 human fibro
7	13.8	57.5	21	6	AX166770	AX166770 Sequence
8	13.8	57.5	32	6	AX044019	AX044019 Sequence
9	13.6	56.7	20	12	AB068316	AB068316 Synthetic
10	13.4	55.8	20	6	AR082336	AR082336 Sequence
11	13.4	55.8	20	6	AR120878	AR120878 Sequence
12	13.4	55.8	20	6	178382	178382 Sequence 18
13	13.4	55.8	37	6	A46389	A46389 Sequence 11
14	13.4	55.8	37	6	AR078965	AR078965 Sequence
15	13.4	55.8	47	6	AX040147	AX040147 Sequence
16	13.4	55.8	51	9	HSCD85701	Z50814 H. sapiens m
17	13.2	55.0	21	6	AB6494	AB6494 Sequence 1
18	13.2	55.0	31	6	177112	177112 Sequence 9
19	13.2	55.0	51	6	AX160359	AX160359 Sequence
20	13	54.2	28	6	AX028853	AX028853 Sequence
21	13	54.2	36	6	A21615	A21615 Oligonucleo
22	13	54.2	45	6	E12626	E12626 PCR primer
23	13	54.2	45	6	E13645	E13645 Primer. 6/1
24	12.8	53.3	30	6	AR028165	AR028165 Sequence
25	12.8	53.3	30	6	AR138695	AR138695 Sequence
26	12.8	53.3	44	6	AX008704	AX008704 Sequence
27	12.8	53.3	46	6	AX008705	AX008705 Sequence
28	12.8	53.3	50	6	AX160360	AX160360 Sequence
29	12.8	53.3	51	6	AX157377	AX157377 Sequence
30	12.8	53.3	51	6	AX157378	AX157378 Sequence
31	12.8	53.3	51	6	AX160873	AX160873 Sequence
32	12.8	53.3	51	6	AX160874	AX160874 Sequence
33	12.8	53.3	51	6	AX160948	AX160948 Sequence
34	12.8	53.3	51	6	AX161486	AX161486 Sequence
35	12.6	52.5	23	6	AR102864	AR102864 Sequence
36	12.6	52.5	23	6	AR129408	AR129408 Sequence
37	12.6	52.5	24	6	136855	136855 Sequence 3
38	12.6	52.5	29	6	E03251	E03251 Synthetic o
39	12.6	52.5	32	6	AR110345	AR110345 Sequence
40	12.6	52.5	42	6	AX166900	AX166900 Sequence
41	12.6	52.5	44	6	A33239	A33239 Synthetic P
42	12.6	52.5	51	6	AX160664	AX160664 Sequence
43	12.4	51.7	25	6	AR157104	AR157104 Sequence
44	12.4	51.7	25	6	AX116636	AX116636 Sequence
45	12.4	51.7	26	6	AX035589	AX035589 Sequence

ALIGNMENTS

RESULT 1
121514
LOCUS 121514
DEFINITION Sequence 61 from patent US 5521300.
ACCESSION 121514
VERSION 121514.1 GI:1601868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Shah,J.S., Nietupski,R.M. and Liu,J.
TITLE Oligonucleotides complementary to mycobacterial nucleic acids
JOURNAL Patent: US 5521300-A 61 28-MAY-1996;
FEATURES
Source location/Qualifiers
1..42
BASE COUNT 13 a 14 c 9 g 6 t
ORIGIN

Query Match	60.88;	Score 14.6;	DB 6;	Length 58,
Basic Local Similarity	81.08;	Pred. No. 6.9e+03;		

PI HHSASHI YASUE YOSHIO KAMARA, SHINICHI SUGIMOTO PC
C12M15/09, C12M1/21, C12M9/12//((C12M15/09, C12R1:125), (C12N1/21, C12R1:19)
PC (C12M9/12, C12R1:19), C12M15/00, (C12M15/00, C12R1:125) CC
FH Key Location/Qualifiers
FT 1. 42
FT source
FT /organism='Artificial Sequence'.

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    /organism="unidentified"
    /db_xref="taxon:32644"
BASE COUNT      14 a      7 c      9 g      12 t
ORIGIN

Query Match
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 aatggaaaacagctgcg 23
    ||||| ||||| ||
Db 12 AATGGAAATYACAGCTGC 30

RESULT 6
HUMACTGM 57 bp mRNA PRI 30-OCT-1994
DEFINITION human fibroblast gamma-actin mRNA, 5' end.
ACCESSION K00791
VERSION K00791.1 GI:178046
KEYWORDS actin; gamma-actin.
SOURCE human fibroblast (simian virus 40-transformed) cdna to mRNA, clone
          phf-gamma-a-1.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 57)
Gunning,P., Ponte,P., Okayama,H., Engel,J., Blau,H. and Kedes,L.
Isolation and characterization of full-length cDNA clones for human
alpha-, beta-, and gamma-actin mRNAs: skeletal but not cytoplasmic
actins have an amino-terminal cysteine that is subsequently removed
Mol. Cell. Biol. 3 (5), 787-795 (1983)
JOURNAL 83244575
MEDLINE

COMMENT [1] also sequenced alpha- and beta-actin mRNAs.
          mature actin has an acidic amino terminus, with alpha-actin, the
          initial translation product has a met-cys preceding this acidic
          amino acid; however, beta- and gamma-actin have only a met
          preceding [1].

FEATURES
  source
    1..57
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /map="17"
  gene
    7..57
    /gene="ACTG1"
  CDS
    7..>57
    /gene="ACTG1"
    /note="gamma-actin"
    /codon_start=1
    /db_xref="GDB:G00-120-536"
    /protein_id="AA51581.1"
    /db_xref="GI:178047"
    /translation="MEEEIALALVIDNGSGMC"
    10..>57
    /gene="ACTG1"
    /note="gamma-actin mature peptide"
BASE COUNT      13 a      15 c      19 g      10 t
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Best Local Similarity 59.2%; Score 14.2; DB 9; Length 57;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 aatggaaaacagctgcg 24
    ||||| || || |||||
Db 6 AATGGAAAGAGATGC 24

RESULT 7

AX166770
LOCUS AX166770 21 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 261 from Patent WO0138503.
ACCESSION AX166770
VERSION AX166770.1 GI:14547045
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 21)
Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clarry,D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 261 31-MAY-2001;
JOURNAL Sugen, Inc. (US)

FEATURES
  source
    1..21
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
BASE COUNT      6 a      6 c      4 g      5 t
ORIGIN

Query Match
Best Local Similarity 57.5%; Score 13.8; DB 6; Length 21;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 tggaaaacagctgcg 24
    ||||| ||||| ||
Db 5 TCCAAAACAGCTGC 21

RESULT 8
AX044019 32 bp DNA PAT 24-NOV-2000
LOCUS AX044019
DEFINITION Sequence 98 from Patent WO0066791.
ACCESSION AX044019
VERSION AX044019.1 GI:11342903
KEYWORDS
SOURCE Neisseria meningitidis.
ORGANISM Neisseria meningitidis
REFERENCE Neisseria meningitidis; beta subdivision; Neisseriaceae;
AUTHORS Neisseria.
1 (bases 1 to 32)
Piazza,M., Hickey,E., Peterson,J., Rettelin,H., Venter,J.C.,
Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
Scarlatto,V., Rappunli,R., Frazer,C.M. and Grandi,G.
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 98 09-NOV-2000;
JOURNAL CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES
  source
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    /organism="Neisseria meningitidis"
    /db_xref="taxon:487"
BASE COUNT      10 a      9 c      6 g      7 t
ORIGIN

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Best Local Similarity 57.5%; Score 13.8; DB 6; Length 32;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 caaatgaaaacagct 20
    ||||| ||||| |||||
Db 10 CATATGAACACAGCT 26

RESULT 9
AB068316 20 bp DNA SYN 08-AUG-2001
LOCUS AB068316
DEFINITION Synthetic construct DNA, forward primer for human STS sts-wt-19810
          at 1p36.

```

ACCESSION AB068316 GI:15129120
VERSION AB068316.1
KEYWORDS
SOURCE synthetic construct DNA.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Matanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohita, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
TITLE A bac-based sts-content map spanning a 35-mb region of human
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
misc_feature /db_xref="taxon:32630"
1..20
/note="forward primer for human STS sts-WI-19810 at 1p36
sts-WI-19810 obtained from clones B33G16, B338N10,
B173013, B249G6, B281E22, B417D2, B452E22, B620C9, B690E2,
B4A4, Human BAC library RPCI-11"
BASE COUNT 8 a 6 c 3 g 3 t
ORIGIN

Query Match 56.7%; Score 13.6; DB 12; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgacaaatggaacacgct 20
||||| ||||||| |||
Db 1 CGACACTTGAAAAACCGCT 20

RESULT 10
AR082336/c 20 bp DNA PAT 31-AUG-2000
LOCUS AR082336
DEFINITION Sequence 180 from patent US 5972704.
ACCESSION AR082336
VERSION AR082336.1 GI:10009062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and
Thompson, J.D.
TITLE HIV nef targeted ribozymes
JOURNAL Patent: US 5972704-A 180 26-OCT-1999;
FEATURES Location/Qualifiers
1..20
source /organism="unknown"
BASE COUNT 3 a 5 c 2 g 10 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aaatggaacacg 19
||||| |||||||
Db 17 AAATGATTAACACG 3

RESULT 11
ARI20878 20 bp DNA PAT 16-MAY-2001
LOCUS ARI20878/c
DEFINITION Sequence 180 from patent US 6159692.
ACCESSION ARI20878
VERSION ARI20878.1 GI:14104454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and
Thompson, J.D.
TITLE Method and reagent for inhibiting human immunodeficiency virus
JOURNAL Patent: US 6159692-A 180 12-DEC-2000;
FEATURES Location/Qualifiers
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source /organism="unknown"
BASE COUNT 3 a 5 c 2 g 10 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aaatggaacacg 19
||||| |||||||
Db 17 AAATGATTAACACG 3

RESULT 12
I78382 20 bp DNA PAT 03-APR-1998
LOCUS I78382
DEFINITION Sequence 180 from patent US 5693535.
ACCESSION I78382
VERSION I78382.1 GI:3014536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and
Thompson, J.D.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 5693535-A 180 02-DEC-1997;
FEATURES Location/Qualifiers
1..20
source /organism="unknown"
BASE COUNT 3 a 5 c 2 g 10 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aaatggaacacg 19
||||| |||||||
Db 17 AAATGATTAACACG 3

RESULT 13
A46389 37 bp DNA PAT 07-MAR-1997
LOCUS A46389
DEFINITION Sequence 11 from Patent WO9523857.
ACCESSION A46389
VERSION A46389.1 GI:2300591
KEYWORDS
SOURCE unidentified.

ORGANISM unidentified
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 37)
TITLE Kerry-Williams,S.M. and Gilbert,S.C.
JOURNAL YEAST STRAINS AND MODIFIED ALBUMINS
COMMENT Patent: WO 9523857-A 11 08-SEP-1995;
DELTA BIOTECHNOLOGY LTD (GB)
FEATURES Other publication AU 1818395 950918.
LOCATION/Qualifiers
SOURCE 1. .37
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 9 g 18 t
ORIGIN

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Best Local Similarity 73.9%; Pred. No. 2.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 gacaaatggaagaacagctgcc 24
||||| ||||| |||||
Db 34 GACAAAACAAAATAAGTCGCAC 12

RESULT 14
AR078965/c 37 bp DNA PAT 31-AUG-2000
LOCUS
DEFINITION Sequence 11 from patent US 5965386.
ACCESSION AR078965
VERSION AR078965.1 GI:10005711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kerry-Williams,S.Martin and Gilbert,S.Catherine.
TITLE Yeast strains and modified albumins
JOURNAL Patent: US 5965386-A 11 12-OCT-1999;
FEATURES Location/Qualifiers
SOURCE 1. .37
/organism="unknown"
BASE COUNT 5 a 5 c 9 g 18 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 37;
Best Local Similarity 73.9%; Pred. No. 2.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 gacaaatggaagaacagctgcc 24
||||| ||||| |||||
Db 34 GACAAAACAAAATAAGTCGCAC 12

RESULT 15
AX040147 47 bp DNA PAT 18-NOV-2000
LOCUS
DEFINITION Sequence 43 from patent WO0063438.
ACCESSION AX040147
VERSION AX040147.1 GI:11230097
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 47)
Gould-Rothberg,B.E. and Rastelli,L.
METHOD of classifying a thyroid carcinoma using differential gene
expression
Patent: WO 0063438-A 43 26-OCT-2000;
Curagen Corporation (US)
FEATURES Location/Qualifiers

SOURCE 1. .47
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 25
BASE COUNT 25 a 7 c 13 g 2 t
ORIGIN

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Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 gacaaatggaagaacagctgcc 24
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Db 18 GAAAAAGGAAAAACAAACCCC 40

Search completed: March 9, 2002, 00:48:33
Job time: 11114 sec

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